```
<110> APPLICANT: MAYER, FRANK
      SCHWIENHORST, ANDREAS
<120> TITLE OF INVENTION: CELL DIGESTION OF BACTERIA
<130> FILE REFERENCE: DREISS-0002
<140> CURRENT APPLICATION NUMBER: US/10/520,145A
<141> CURRENT FILING DATE: 2005-01-03
<150> PRIOR APPLICATION NUMBER: PCT/EP03/007068
<151> PRIOR FILING DATE: 2003-07-02
<150> PRIOR APPLICATION NUMBER: DE 10229645.6
<151> PRIOR FILING DATE: 2002-07-02
<160> NUMBER OF SEQ ID NOS: 14
<170> SOFTWARE: PatentIn Ver. 3.3
<210> SEO ID NO 1
<211> LENGTH: 4527
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: EF-Tu-GFP-His
      of vector pEGFP
<400> SEQUENCE: 1
      agegeceaat aegeaaaceg ceteteceeg egegttggee gatteattaa tgeagetgge 60
      acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
      teacteatta ggeacceag getttacact ttatgettee ggetegtatg ttgtgtggaa 180
      ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
      catgorigea geatgtotaa agaaaaattt gaacgtacaa aaccgcacgt taacgttggt 300
      actateggee acgttgacca eggtaaaact actetgaccg etgeaateac caccgtactg 360
      getaaaacet acggeggtge tgetegtgea ttegaceaga tegataacge geeggaagaa 420
      aaagetegtg gtateaceat caacaettet caegttgaat acgacaecee gaecegteac 480
      tacgcacacg tagactgccc ggggcacgcc gactatgtta aaaacatgat caccggtgct 540
      getcagatgg acggcgcgat cetggtagtt getgcgactg acggcccgat gecgcagact 600
      cotgaggaga tectootggg tegteaggta ggcgtteegt acateategt gtteetgaac 660
      aaatgcgaca tggttgatga cgaagagctg ctggaactgg ttgaaatgga agttcgtgaa 720
      ettetgtete agtacgaett eeegggegae gacacteega tegttegtgg ttetgetetg 780
      aaagggetgg aaggcgacge agagtgggaa gcgaaaatee tggaactgge tggetteetg 840
      gattettata tteeggaace agagegtgeg attgacaage egtteetget geegategaa 900
      gacgtattet ccateteegg tegtggtace gttgttaceg gtegtgtaga acgeggtate 960
      atcaaaqttq qtqaaqaaqt tqaaatcqtt qqtatcaaaq aqactcaqaa qtctacctqt 1020
      actggcgttg aaatgttccg caaactgctg gacgaaggcc gtgctggtga gaacgtaggt 1080
      gttctgctgc gtggtatcaa acgtgaagaa atcgaacgtg gtcaggtact ggctaagccg 1140
      ggcaccatca agccgcacac caagttcgaa tctgaagtgt acattctgtc caaagatgaa 1200
      ggcggccgtc atactccgtt cttcaaaggc taccgtccgc agttctactt ccgtactact 1260
      gacgtgactg gtaccatcga actgccggaa ggcgtagaga tggtaatgcc gggcgacaac 1320
      atcaaaatgg ttgttaccct gatccacccg atcgcgatgg acgacggtct gcgtttcgca 1380
      atcogtgaag goggcogtac cgttggogog ggogttgtag ctaaagttct gggcaagctt 1440
      accatggtga gcaagggcga ggagctgttc accggggtgg tgcccatcct ggtcgagctg 1500
      gacggcgacg taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc 1560
      tacggcaagc tgaccctgaa gttcatctgc accaccggca agctgcccgt gccctggccc 1620
      accetegtga ceaccetgae etacggegtg eagtgettea geogetacce egaccacatg 1680
      aagcagcacg acttetteaa gteegeeatg eeegaagget aegteeagga gegeaceate 1740
      ttetteaagg acgacggeaa ctacaagace cgcgcgagg tgaagttega gggcgacace 1800
      ctgqtqaacc gcatcgagct gaagggcatc gacttcaagg aggacggcaa catcctgggg 1860
      cacaagetgg agtacaacta caacagecac aacgtetata teatggeega caageagaag 1920
      aacqqcatca aqqtqaactt caaqatccqc cacaacatcq aqqacqqcaq cqtqcaqctc 1980
      geogaceact accageagaa caceeceate ggegaeggee cegtgetget geoegacaae 2040
      cactacetga geacceagte egecetgage aaagaceeca aegagaageg egateacatg 2100
      gtcctgctgg agttcgtgac cgccqccggg atcactctcg gcatggacga gctgtacaag 2160
      etteateace ateaceatea etaactgtae aagtaagaat eecaactgag egeeggtege 2220
      taccattacc aacttqtctq qtqtcaaaaa taataqqcct actaqtcqqc cqtacqqqcc 2280
```

```
ctttcqtctc gcgcqtttcq gtgatgacgg tgaaaacctc tgacacatge agctcccqga 2340
gacggtcaca gcttgtctgt aagcggatgc cgggagcaga caagcccgtc agggcgcgtc 2400
aggggtgtt gggggtgtc ggggctggct taactatgcg gcatcagagc agattgtact 2460
gagagtqcac catatqcqqt qtqaaatacc qcacaqatqc qtaaqqaqaa aataccqcat 2520
caggoggeet taagggeete gtgatacgee tatttttata ggttaatgte atgataataa 2580
tggtttetta gaegteaggt ggeaetttte ggggaaatgt gegeggaace cetatttgtt 2640
tatttttcta aatacattca aatatgtatc cgctcatgag acaataaccc tgataaatgc 2700
ttcaataata ttgaaaaagg aagagtatga gtattcaaca tttccgtgtc gcccttattc 2760
ccttttttqc qqcattttqc cttcctqttt ttqctcaccc aqaaacqctq qtgaaaqtaa 2820
aagatgetga agateagttg ggtgeacgag tgggttacat egaactggat eteaacageg 2880
gtaagateet tgagagtttt egeeegaag aaegttttee aatgatgage aettttaaag 2940
ttetgetatg tggegegta ttatecegta ttgacgeegg geaagageaa eteggtegee 3000
gcatacacta ttctcagaat gacttggttg agtactcacc agtcacagaa aagcatctta 3060
cggatggcat gacagtaaga gaattatgca gtgctgccat aaccatgagt gataacactg 3120
eggecaactt acttetgaca acquteggag gacegaagga getaaceget tttttgcaca 3180
acatggggga tcatgtaact cgccttgatc gttgggaacc ggagctgaat gaagccatac 3240
caaacgacga gcgtgacacc acgatgcctg tagcaatggc aacaacgttg cgcaaactat 3300
taactggcga actacttact ctagetteec ggcaacaatt aatagactgg atggaggcgg 3360
ataaagttgc aggaccactt ctgcgctcgg cccttccggc tggctggttt attgctgata 3420
aatctggage eggtgagegt gggtetegeg gtateattge ageaetgggg ecagatggta 3480
ageceteeeg tategtagtt atetacaega eggggagtea ggeaactatg gatgaaegaa 3540
atagacagat cgctgagata ggtgcctcac tgattaagca ttggtaactg tcagaccaag 3600
tttactcata tatactttag attgatttaa aacttcattt ttaatttaaa aggatctagg 3660
tgaagateet ttttgataat eteatgacea aaateeetta aegtgagttt tegtteeact 3720
gagegteaga eccegtagaa aagateaaag gatettettg agateettt titetgegeg 3780
taatctqctq cttqcaaaca aaaaaaccac cqctaccaqc qqtqqtttqt ttqccqqatc 3840
aagagctacc aactettttt ccgaaggtaa ctggetteag cagagcgeag ataccaaata 3900
etgteettet agtgtageeg tagttaggee accaetteaa gaactetgta geacegeeta 3960
catacetege tetgetaate etgttaceag tggetgetge cagtggegat aagtegtgte 4020
ttaccgggtt ggactcaaga cgatagttac cggataaggc gcagcggtcg ggctgaacgg 4080
ggggttcgtg cacacagccc agcttggagc gaacgaccta caccgaactg agatacctac 4140
agogtgaget atgagaaage gecaegette eegaagggag aaaggeggae aggtateegg 4200
taagcggcag ggtcggaaca ggagagcgca cgagggagct tccaggggga aacgcctggt 4260
atetttatag teetgteggg tttegeeace tetgaettga gegtegattt ttgtgatget 4320
cgtcaggggg gcggagccta tggaaaaacg ccagcaacgc ggccttttta cggttcctgg 4380
cettttgetg geettttget cacatgttet tteetgegtt ateceetgat tetgtggata 4440
acceptattac egectttgag tgagetgata eegetegeeg eageegaacg accepagegea 4500
gcgagtcagt gagcgaggaa gcggaag
                                                                  4527
```

- <210> SEQ ID NO 2 <211> LENGTH: 3651
- <212> TYPE: DNA
- <213> ORGANISM: Artificial Sequence
- <220> FEATURE:
- <223> OTHER INFORMATION: Description of Artificial Sequence: Domain 3 of EF-Tu-GFP-His of vector pEGFP

<400> SEQUENCE: 2

agogocoaat acgoaaacc cototococ gogottgoc gattaattaa tgagattaq 20 acgoaagtat tecqaattag aaagoggaga gtagagogaa gogaattaattaa tgagattaga 120 toatoatta ggoacocoag gotttacact ttatgettee ggotogtatg ttgttgtggaa 180 ttgttgagogg ataacaattt cacacaggaa acaagottaga coatgattag cocaagottag 240 catgoctgaa gogotaagoc ggogocoaca caagottaga atcgaagtg 300 tacattottgt cocaagattag agogocogt catactocgt tottoaaagg ctacoctcog 360 cagtistact tecgtactac tgaogtgact ggacaca caagttaga 420 atggtaatge cggogocaa catocaagat ggacagaa gudogaaga 420 atggtaatge cggogocaa catocaaaatg gttgttacoc tgatocacce gatogoga ggacgacaa catocaaaatg gttgttacoc tgatocacce gatogoga gggottgta 540 gocaaaggtt tgggottgoca gottagocag gggogottac coctagoga Gudogaaggogo gottagacga gogagaaca catocaatg gtggacagaa gogaagact gttacacgg 600 gtggtgocoa toctggtoga gottgacoga gogogaacce toctggtoga gottgacoga gogoagaac cacaagatt cagogttgococa cocaagatt cagogttgococacacce 720

```
ggcaagetge cegtgeeetg geccaecete gtgaccaece tgacctaegg egtgeagtge 780
ttcagccgct accccgacca catgaagcag cacgacttct tcaagtccgc catgcccgaa 840
ggctacqtcc aggagggcac catcttcttc aaggacgacg gcaactacaa gacccgcgcc 900
gaggtgaagt tegaggega caccetggtg aaccgcateg agetgaaggg categactte 960
aaggaggacg gcaacatect ggggcacaag ctggagtaca actacaacag ccacaacgtc 1020
tatatcatgq ccgacaaqca qaaqaacggc atcaaqqtqa acttcaaqat ccqccacaac 1080
ategaggaeg geagegtgea getegeegae caetaceage agaacacece categgegae 1140
ggccccqtqc tqctqcccqa caaccactac ctqaqcaccc aqtccqccct qaqcaaaqac 1200
cccaacgaga agcgcgatca catggtcctg ctggagttcg tgaccgccgc cgggatcact 1260
cteggeatgg acgagetgta caagetteat caccateace atcactaact gtacaagtaa 1320
gaateecaac tgagegeegg tegetaceat taccaacttg tetggtgtca aaaataatag 1380
geetactagt eggeegtacg ggeeettteg tetegegegt tteggtgatg acggtgaaaa 1440
cetetqacae atgeagetce eggagaeggt cacagettgt etgtaagegg atgeegggag 1500
cagacaagee egtcagggeg egtcageggg tgttggeggg tgtegggget ggettaacta 1560
tgcggcatca gagcagattg tactgagagt gcaccatatg cggtgtgaaa taccgcacag 1620
atgcgtaagg agaaaatacc gcatcaggcg gccttaaggg cctcgtgata cgcctatttt 1680
tataggttaa tgtcatgata ataatggttt cttagacgtc aggtggcact tttcggggaa 1740
atgtgcgcgg aacccctatt tgtttatttt tctaaataca ttcaaatatg tatccgctca 1800
tgagacaata accetgataa atgetteaat aatattgaaa aaggaagagt atgagtatte 1860
aacattteeg tgtegeeett atteeetttt ttgeggeatt ttgeetteet gtttttgete 1920
acccagaaac gctggtgaaa gtaaaagatg ctgaagatca gttgggtgca cgagtgggtt 1980
acategaact ggateteaac ageggtaaga teettgagag ttttegeece gaagaacgtt 2040
ttccaatgat gagcactttt aaagttctgc tatgtggcgc ggtattatcc cgtattgacg 2100
cogggcaaga gcaactoggt cgccgcatac actattotca gaatgacttg gttgagtact 2160
caccagtcac agaaaagcat cttacggatg gcatgacagt aagagaatta tgcagtgctg 2220
ccataaccat gagtgataac actgcggcca acttacttct gacaacgatc ggaggaccga 2280
aggagetaac egettttttg cacaacatgg gggateatgt aactegeett gategttggg 2340
aaccggaget gaatgaagec ataccaaacg acgagegtga caccacgatg cetgtageaa 2400
tggcaacaac gttgcgcaaa ctattaactg gcgaactact tactctagct tcccggcaac 2460
aattaataga ctggatggag gcggataaag ttgcaggacc acttctgcgc tcggcccttc 2520
eggetggetg gtttattget gataaatetg gageeggtga gegtgggtet egeggtatea 2580
ttgcagcact ggggccagat ggtaagccct cccgtatcgt agttatctac acgacgggga 2640
gtcaggcaac tatggatgaa cgaaatagac agatcgctga gataggtgcc tcactgatta 2700
agcattgqta actgtcagac caagtttact catatatact ttagattgat ttaaaacttc 2760
atttttaatt taaaaggatc taggtgaaga teetttttga taateteatg accaaaatee 2820
cttaacqtqa qttttcqttc cactqaqcqt caqaccccqt aqaaaaqatc aaaqqatctt 2880
cttgagatcc tttttttctg cgcgtaatct gctgcttgca aacaaaaaaa ccaccgctac 2940
cagoggtggt ttgtttgccg gatcaagagc taccaactct ttttccgaag gtaactggct 3000
teagragage gragatacea aatactgtee ttetagtgta geogtagtta ggecaccact 3060
toaagaacto tgtagcaccg cotacataco togototgot aatootgtta coagtggotg 3120
ctgccagtgg cgataagtcg tgtcttaccg ggttggactc aagacgatag ttaccggata 3180
aggogoagcg gtogggotga acggggggtt cgtgcacaca gcccagcttg gagcgaacga 3240
cctacaccga actgagatac ctacagcgtg agctatgaga aagcgccacg cttcccgaag 3300
ggagaaaggc ggacaggtat ccggtaagcg gcagggtcgg aacaggagag cgcacgaggg 3360
agetteeagg gggaaacgee tggtatettt atagteetgt egggtttege eacetetgae 3420
ttgagcgtcg atttttgtga tgctcgtcag gggggcggag cctatggaaa aacgccagca 3480
acgoggett tttacggttc ctggcetttt getggcettt tgetcacatg ttettteetg 3540
egttateece tgattetgtg gataacegta ttacegeett tgagtgaget gatacegete 3600
geograged aacqaeeqaq eqeaqeqaqt caqtqaqeqa qqaaqeqqaa q
                                                                  3651
```

<210> SEQ ID NO 3 <211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

 $<\!\!223\!\!>$ OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

```
<210> SEO ID NO 4
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2)..(28)
<400> SEQUENCE: 4
      g tac aag ctt cat cac cat cac cat cac taactgtaca agtaag
                                                                        44
        Tyr Lys Leu His His His His His
<210> SEQ ID NO 5
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide
<400> SEQUENCE: 5
      ttcgaagtag tggtagtggt agtgattgac atgttcattc ttaa
                                                                         44
<210> SEQ ID NO 6
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<400> SEQUENCE: 6
      Tvr Lvs Leu His His His His His His
<210> SEQ ID NO 7
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(21)
<400> SEQUENCE: 7
                                                                         21
      act age tgc age atg tet aaa
      Thr Ser Cys Ser Met Ser Lys
<210> SEO ID NO 8
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

peptide

```
<400> SEQUENCE: 8
      Thr Ser Cvs Ser Met Ser Lvs
<210> SEO ID NO 9
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(21)
<400> SEQUENCE: 9
                                                                         21
      ctg ggc aag ctt acc atg gtg
      Leu Gly Lys Leu Thr Met Val
<210> SEO ID NO 10
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<400> SEQUENCE: 10
      Leu Gly Lys Leu Thr Met Val
<210> SEQ ID NO 11
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(21)
<400> SEQUENCE: 11
      act age tge age get aag eeg
                                                                         21
      Thr Ser Cys Ser Ala Lys Pro
<210> SEO ID NO 12
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<400> SEOUENCE: 12
      Thr Ser Cys Ser Ala Lys Pro
       1
<210> SEQ ID NO 13
<211> LENGTH: 24
<212> TYPE: DNA
```

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
     oligonucleotide
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(24)
<400> SEQUENCE: 13
      ctg ggc tgc aag ctt acc atg gtg
                                                                        24
      Leu Gly Cys Lys Leu Thr Met Val
<210> SEQ ID NO 14
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
     peptide
<400> SEQUENCE: 14
      Leu Gly Cys Lys Leu Thr Met Val
```